

2621

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant(s): Eric T. BALDWIN et al.

Serial No.: 09/896,580
Confirmation No.: 7868

Filed: 29 June 2001



Group Art Unit: 2621

Examiner: Unknown

Docket No.: 6317.N

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Technology Center 2600

Title: CRYSTALLIZATION AND STRUCTURE OF STAPHYLOCOCCUS AUREUS PEPTIDE DEFORMYLASE

Assistant Commissioner for Patents
Washington, D.C. 20231

We are transmitting the following documents along with this Transmittal Sheet (which is submitted in triplicate):

An itemized return postcard.
 A Petition for Extension of Time for ___ month(s) and a check in the amount of \$___ for the required fee.
 An Information Disclosure Statement (2 pgs); 1449 forms (5 pgs); and copies of 61 documents cited on the 1449 forms (**MAILED IN 2 BOXES**).
 A check in the amount of \$___, for ___.
 A certified copy of a ___ application, Serial No. ___, filed _____, the right of priority of which is claimed under 35 U.S.C. §119.
 Other:
 Amendment ___ No Additional fee is required. ___ The fee has been calculated as shown:

Fee Calculation for Claims Pending After Amendment					
	Pending Claims after Amendment (1)	Claims Paid for Earlier (2)	Number of Additional Claims (1-2)	Cost per Additional Claim	Additional Fees Required
Total Claims				x \$18 =	
Independent Claims				x \$84 =	
One or More New Multiple Dependent Claims Presented? If Yes, Add \$280 Here →					
Total Additional Claim Fees Required					

Please consider this a PETITION FOR EXTENSION OF TIME for a sufficient number of months to enter these papers and please charge any additional fees or credit overpayment to Deposit Account No. 13-4895. Triplicate copies of this sheet are enclosed.

CERTIFICATE UNDER 37 C.F.R. §1.8: The undersigned hereby certifies that this Transmittal Letter and the paper(s), as described hereinabove, are being deposited in the United States Postal Service, as first class mail, in an envelope addressed to: Assistant Commissioner for Patents, Washington, D.C. 20231, on this 6/12 day of December, 2001.

MUETING, RAASCH & GEBHARDT, P.A.
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(LARGE ENTITY TRANSMITTAL UNDER RULE 1.8)



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PATENT
Docket No. 6317.N

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant(s): Eric T. BALDWIN et al.) Group Art Unit: 2621
)
Serial No.: 09/896,580) Examiner: Unknown
Confirmation No.: 7868)
)
Filed: 29 June 2001)
)
For: CRYSTALLIZATION AND STRUCTURE OF *STAPHYLOCOCCUS AUREUS*
PEPTIDE DEFORMYLASE

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INFORMATION DISCLOSURE STATEMENT

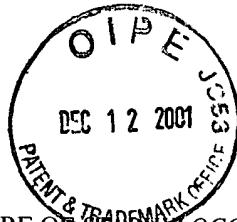
Assistant Commissioner for Patents
Washington D.C. 20231

Sir:

In compliance with the duty imposed by 37 C.F.R. § 1.56, and in accordance with C.F.R. §§ 1.97 *et. seq.*, the materials enclosed herewith are brought to the attention of the Examiner as possibly being of interest in connection with the above-identified patent application. Consideration of each of the documents listed on the attached 1449 forms is respectfully requested. Pursuant to the provisions of M.P.E.P. §609, Applicants further request that a copy of the 1449 forms, marked as being considered and initialed by the Examiner, be returned with the next Official Communication.

It is believed that no fee is due, as this Information Disclosure Statement is filed prior to the receipt of any Action on the merits. However, in the event a fee is due, please charge any fee or credit any overpayment to Account No. 13-4895.

Information Disclosure Statement
Applicant(s): Eric T. BALDWIN et al.
Serial No.: 09/896,580
Confirmation No.: 7868
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For: CRYSTALLIZATION AND STRUCTURE OF STAPHYLOCOCCUS AUREUS PEPTIDE DEFORMYLASE



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The Examiner is invited to contact Applicants' Representatives at the below-listed telephone number, if they can be of any assistance during prosecution of the present application.

Respectfully submitted for

Eric T. Baldwin et al.

By

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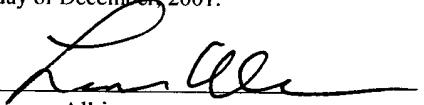
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The undersigned hereby certifies that this paper is being deposited in the United States Postal Service, as first class mail, in an envelope addressed to: Assistant Commissioner for Patents, Washington, D.C. 20231, on this 6th day of December, 2001.


Loren Albin

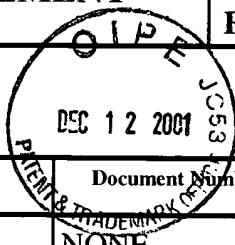
December 6, 2001
Date

By:


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**INFORMATION
DISCLOSURE
STATEMENT**

Atty. Docket No.: 6317.N	Serial No.: 09/896,580
Applicant(s): Eric T. BALDWIN et al.	Confirmation No.: 7868
Filing Date: 29 June 2001	Group: 2621

**U.S. PATENT DOCUMENTS**

Examiner Initial		Document Number	Date	Name	Class	Subclass	Filing Date If Appropriate
		NONE					

FOREIGN PATENT DOCUMENTS

Examiner Initial		Document Number	Date	Country	Class	Subclass	Translation	
							Yes	No
		0 786 519 A2, A3	07/30/98	EPO				
		WO 99/47639	09/23/99	WIPO			RECEIVED	
		WO 99/47662	09/23/99	WIPO			DEC 14 2001	
		WO 00/12678	03/09/00	WIPO			Technology Center 2600	
		WO 01/16292	03/23/00	WIPO				

OTHER DOCUMENTS (Including Authors, Title, Date, Pertinent Papers, etc.)

Examiner Initial	Document Description
	Adams, "On the Release of the Formyl Group from Nascent Protein," <i>Journal of Molecular Biology</i> , 33(3):571-589 (1968).
	Ball et al., "Cleavage of the N-terminal Formylmethionine Residue from a Bacteriophage Coat Protein <i>in vitro</i> ," <i>Journal of Molecular Biology</i> , 79(3):531-537 (1973).
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	Benson et al., "An enzyme-substrate complex involved in bacterial cell wall biosynthesis," <i>Nature Structural Biology</i> , 2(8):644-653 (1995).
	BLAST 2 Sequences. [online] National Center for Biotechnology Information, National Institutes of Health, United States, [retrieved 2001-08-29]. Retrieved from the Internet: <URL: http://www.ncbi.nlm.nih.gov/gorf/bl2.html >, 1 page.
	Blundell et al., <i>Protein Crystallography</i> , Academic Press, New York, NY, Title page, publication page and table of contents only, 8 pages (1976).

EXAMINER	Date Considered

*Examiner: Initial if citation considered, whether or not citation is in conformance with MPEP 609; Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant.

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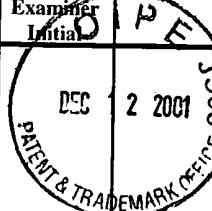
Examiner Initial		Document Description
O I P E JU53	DEC 12 2001	Blundell, "Metalloproteinase superfamilies and drug design," <i>Nature Structural Biology</i> , 1(2):73-75 (1994).
		Böhm, "The computer program LUDI: A new method for the de novo design of enzyme inhibitors," <i>Journal of Computer-Aided Molecular Design</i> , 6(1):61-78 (1992).
		Brünger, "Extension of Molecular Replacement: a New Search Strategy based on Patterson Correlation Refinement," <i>Acta Crystallographica</i> , A46:46-57 (1990).
		Brünger, <i>X-PLOR Version 3.1: A System for X-ray Crystallography and NMR</i> , Yale University Press, New Haven, Title page, publication page and table of contents only, 13 pages (1992).
Technology Center 2600	RECEIVED DEC 14 2001	Chan et al., "Crystal Structure of the <i>Escherichia coli</i> Peptide Deformylase," <i>Biochemistry</i> , 36(45):13904-13909 (1997).
		Collaborative Computational Project, Number 4, SERC Daresbury Laboratory, "The CCP4 Suite: Programs for Protein Crystallography," <i>Acta Crystallographica</i> , D50(5):760-763 (1994).
		Dalbøge et al., "In vivo processing of N-terminal methionine in <i>E. coli</i> ," <i>FEBS Letters</i> , 266(1,2):1-3 (1990).
		Eisen et al., "HOOK: A Program for Finding Novel Molecular Architectures That Satisfy the Chemical and Steric Requirements of a Macromolecule Binding Site," <i>Proteins: Structure, Function, and Genetics</i> , 19(3):199-221 (1994).
		Finzel, "LORE: Exploiting Database of Known Structures," <i>Methods in Enzymology</i> , 277:230-242 (1997).
		Gillet et al., "SPROUT: A program for structure generation," <i>Journal of Computer-Aided Molecular Design</i> , 7(2):127-153 (1993).
		Goodford, "A Computational Procedure for Determining Energetically Favorable Binding Sites on Biologically Important Macromolecules," <i>Journal of Medicinal Chemistry</i> , 28(7):849-857 (1985).
		Goodsell et al., "Automated Docking of Substrates to Proteins by Simulated Annealing," <i>Proteins: Structure, Function, and Genetics</i> , 8(3):195-202 (1990).
		Hao et al., "Structural Basis for the Design of Antibiotics Targeting Peptide Deformylase," <i>Biochemistry</i> , 38(15):4712-4719 (1999).

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Examiner Initials 	Document Description
	Hendrickson et al., "Stereochemically Restrained Crystallographic Least-Squares Refinement of Macromolecule Structures," in <i>Biomolecular Structure, Conformation, Function, and Evolution</i> , Srinivasan, ed., Pergamon Press Ltd., Oxford, UK, Title page, publication page and pages 43-57 (1981).
	Hirel et al., "Genetic engineering of methionyl-tRNA synthetase: <i>in vitro</i> regeneration of an active synthetase by proteolytic cleavage of a methionyl-tRNA synthetase-β-galactosidase chimeric protein," <i>Biochimie</i> , 70(6):773-782 (1988).
	Hirel et al., "Extent of N-terminal methionine excision from <i>Escherichia coli</i> proteins is governed by the side-chain length of the penultimate amino acid," <i>Proceedings of the National Academy of Sciences, USA</i> , 86(21):8247-8251 (1989).
	Jancarik et al., "Sparse matrix sampling: a screening method for crystallization of proteins," <i>Journal of Applied Crystallography</i> , 24(4):409-411 (1991).
	Jongeneel et al., "A unique signature identifies a family of zinc-dependent metallopeptidases," <i>FEBS Letters</i> , 242(2):211-214 (1989).
	Kozak, "Comparison of Initiation of Protein Synthesis in Prokaryotes, Eucaryotes, and Organelles," <i>Microbiological Reviews</i> , 47(1):1-45 (1983).
	Kraulis, "MOLSCRIPT: a program to produce both detailed and schematic plots of protein structures," <i>Journal of Applied Crystallography</i> , 24(5):946-950 (1991).
	Kuntz et al., "A Geometric Approach to Macromolecule-Ligand Interactions," <i>Journal of Molecular Biology</i> , 161(2):269-288 (1982).
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	Lattman, "Use of the Rotation and Translation Functions," <i>Methods in Enzymology</i> , 115:55-77 (1985).
	Lauri et al., "CAVEAT: A program to facilitate the design of organic molecules," <i>Journal of Computer-Aided Molecular Design</i> , 8(1):51-66 (1994).
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		Martin, "3D Database Searching in Drug Design," <i>Journal of Medicinal Chemistry</i> , 35(12):2145-2154 (1992). <i>RECEIVED</i>
DEC 12 2001		Matthews, "Structural Basis of the Action of Thermolysin and Related Zinc Peptidases," <i>Accounts of Chemical Research</i> , 21:333-340 (1988).
		Mazel et al., "Genetic characterization of polypeptide deformylase, a distinctive enzyme of eubacterial translation," <i>The EMBO Journal</i> , 13(4):914-923 (1994).
		Meinnel et al., "The <i>Escherichia coli</i> <i>fmt</i> Gene, Encoding Methionyl-tRNA ^{MET} Formyltransferase, Escapes Metabolic Control," <i>Journal of Bacteriology</i> , 175(4):993-1000 (1993).
Technology Center 2600	DEC 14 2001 <i>RECEIVED</i>	Meinnel et al., "Enzymatic Properties of <i>Escherichia coli</i> Peptide Deformylase," <i>Journal of Bacteriology</i> , 177(7):1883-1887 (1995).
		Meng et al., "Automated Docking with Grid-Based Energy Evaluation," <i>Journal of Computational Chemistry</i> , 13(4):505-524 (1992).
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		Miranker et al., "Functionality Maps of Binding Sites: A Multiple Copy Simultaneous Search Method," <i>Proteins: Structure, Function, and Genetics</i> , 11(1):29-34 (1991).
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		Rossmann, ed., <i>The Molecular Replacement Method A Collection of Papers on the Use of Non-Crystallographic Symmetry</i> , Gordon & Breach, Science Publishers, Inc., New York, Title page, publication page, and table of contents only, 6 pages (1972).

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O P E		Sack, "CHAIN - A Crystallographic Modeling Program," <i>Journal of Molecular Graphics</i> , 6(4):224-225 (1988).
DEC 12 2001		Schechter et al., "On the size of the active site in proteases. I. Papain," <i>Biochemical and Biophysical Research Communications</i> , 27(2):157-162 (1967).
PATENT & TRADEMARK OFFICE		Schmitt et al., "Molecular recognition governing the initiation of translation in <i>Escherichia coli</i> . A review," <i>Biochimie</i> , 78(7):543-554 (1996).
		Schulman et al., "Anticodon loop size and sequence requirements for recognition of formylmethionine tRNA by methionyl-tRNA synthetase," <i>Proceedings of the National Academy of Sciences, USA</i> , 80(22):6755-6759 (1983).
Technology Center 2600	RECEIVED	Sheldrick et al., "Structure Solution by Iterative Peaklist Optimization and Tangent Expansion in Space Group P1," <i>Acta Crystallographica</i> , B51(4):423-431 (1995).
DEC 14 2001		Solbiati et al., "Processing of the N Termini of Nascent Polypeptide Chains Requires Deformylation Prior to Methionine Removal," <i>Journal of Molecular Biology</i> , 290(3):607-614 (1999).
		Tatusova et al., "BLAST 2 Sequences, a new tool for comparing protein and nucleotide sequences," <i>FEMS Microbiology Letters</i> , 174(2):247-250 (1999).
		Travis, "Proteins and Organic Solvents Make an Eye-Opening Mix," <i>Science</i> , 262(5138):1374 (1993).
		Van Duyne et al., "Atomic Structures of the Human Immunophilin FKBP-12 Complexes with FK506 and Rapamycin," <i>Journal of Molecular Biology</i> , 229(1):105-124 (1993).
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		Wyckoff et al., eds., "Diffraction Methods for Biological Macromolecules, Part A," <i>Methods in Enzymology</i> , volume 114, Title page, publication page and table of contents only, 3 pages (1985).
		Wyckoff et al., eds., "Diffraction Methods for Biological Macromolecules, Part B," <i>Methods in Enzymology</i> , volume 115, Title page, publication page and table of contents only, 3 pages (1985).

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